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## SEQUENCE LISTING

TECH CENTER 1600/2900

<110> Luo, Yin  
Chan, Evan  
Xu, Xiang  
Huang, Betty

<120> Tankyrase H, Compositions Involved in the Cell Cycle and Methods of Use

<130> A-68292-2/RMS/DHR

<140> US 09/843,159

<141> 2001-04-25

<150> US 09/696,668

<151> 2000-10-25

<150> US 09/427,154

<151> 1999-10-25

<160> (17)

<170> PatentIn version 3.1

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Lys Ser Thr Pro Leu His Leu Ala Ala Gly Tyr Asn Arg Val Lys Ile  
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Val Gln Leu Leu Leu Gln His Gly Ala Asp Val His Ala Lys Asp Lys  
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Gly Asp Leu Val Pro Leu His Asn Ala Cys Ser Tyr Gly His Tyr Glu  
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Val Thr Glu Leu Leu Val Lys His Gly Ala Cys Val Asn Ala Met Asp  
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Leu Gln His Gly Ala Asp Val His Ala Lys Asp Lys Gly Asp Leu Val  
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Cys Arg Asp Ile Glu Gly Arg Gln Ser Thr Pro Leu His Phe Ala Ala  
595 600 605

Gly Tyr Asn Arg Val Ser Val Val Glu Tyr Leu Leu Gln His Gly Ala  
610 615 620

Asp Val His Ala Lys Asp Lys Gly Gly Leu Val Pro Leu His Asn Ala  
625 630 635 640

Cys Ser Tyr Gly His Tyr Glu Val Ala Glu Leu Leu Val Lys His Gly  
645 650 655

Ala Val Val Asn Val Ala Asp Leu Trp Lys Phe Thr Pro Leu His Glu  
660 665 670

Ala Ala Ala Lys Gly Lys Tyr Glu Ile Cys Lys Leu Leu Leu Gln His  
675 680 685

Gly Ala Asp Pro Thr Lys Lys Asn Arg Asp Gly Asn Thr Pro Leu Asp  
690 695 700

Leu Val Lys Asp Gly Asp Thr Asp Ile Gln Asp Leu Leu Arg Gly Asp  
705 710 715 720

Ala Ala Leu Leu Asp Ala Ala Lys Lys Gly Cys Leu Ala Arg Val Lys  
725 730 735

Lys Leu Ser Ser Pro Asp Asn Val Asn Cys Arg Asp Thr Gln Gly Arg  
740 745 750

His Ser Thr Pro Leu His Leu Ala Ala Gly Tyr Asn Asn Leu Glu Val  
755 760 765

Ala Glu Tyr Leu Leu Gln His Gly Ala Asp Val Asn Ala Gln Asp Lys  
770 775 780

Gly Gly Leu Ile Pro Leu His Asn Ala Ala Ser Tyr Gly His Val Asp  
785 790 795 800

Val Ala Ala Leu Leu Ile Lys Tyr Asn Ala Cys Val Asn Ala Thr Asp  
805 810 815

25  
Cont.

Lys Trp Ala Phe Thr Pro Leu His Glu Ala Ala Gln Lys Gly Arg Thr  
820 825 830

Gln Leu Cys Ala Leu Leu Leu Ala His Gly Ala Asp Pro Thr Leu Lys  
835 840 845

Asn Gln Glu Gly Gln Thr Pro Leu Asp Leu Val Ser Ala Asp Asp Val  
850 855 860

Ser Ala Leu Leu Thr Ala Ala Met Pro Pro Ser Ala Leu Pro Ser Cys  
865 870 875 880

Tyr Lys Pro Gln Val Leu Asn Gly Val Arg Ser Pro Gly Ala Thr Ala  
885 890 895

Asp Ala Leu Ser Ser Gly Pro Ser Ser Pro Ser Ser Leu Ser Ala Ala  
900 905 910

Ser Ser Leu Asp Asn Leu Ser Gly Ser Phe Ser Glu Leu Ser Ser Val  
915 920 925

Val Ser Ser Ser Gly Thr Glu Gly Ala Ser Ser Leu Glu Lys Lys Glu  
930 935 940

Val Pro Gly Val Asp Phe Ser Ile Thr Gln Phe Val Arg Asn Leu Gly  
945 950 955 960

Leu Glu His Leu Met Asp Ile Phe Glu Arg Glu Gln Ile Thr Leu Asp  
965 970 975

Val Leu Val Glu Met Gly His Lys Glu Leu Lys Glu Ile Gly Ile Asn  
980 985 990

Ala Tyr Gly His Arg His Lys Leu Ile Lys Gly Val Glu Arg Leu Ile  
995 1000 1005

Ser Gly Gln Gln Gly Leu Asn Pro Tyr Leu Thr Leu Asn Thr Ser  
1010 1015 1020

Gly Ser Gly Thr Ile Leu Ile Asp Leu Ser Pro Asp Asp Lys Glu  
1025 1030 1035

Phe Gln Ser Val Glu Glu Glu Met Gln Ser Thr Val Arg Glu His  
1040 1045 1050

Arg Asp Gly Gly His Ala Gly Gly Ile Phe Asn Arg Tyr Asn Ile

1055		1060		1065
Leu Lys Ile Gln Lys Val Cys Asn Lys Lys Leu Trp Glu Arg Tyr				
1070		1075		1080
Thr His Arg Arg Lys Glu Val Ser Glu Glu Asn His Asn His Ala				
1085		1090		1095
Asn Glu Arg Met Leu Phe His Gly Ser Pro Phe Val Asn Ala Ile				
1100		1105		1110
Ile His Lys Gly Phe Asp Glu Arg His Ala Tyr Ile Gly Gly Met				
1115		1120		1125
Phe Gly Ala Gly Ile Tyr Phe Ala Glu Asn Ser Ser Lys Ser Asn				
1130		1135		1140
Gln Tyr Val Tyr Gly Ile Gly Gly Gly Thr Gly Cys Pro Val His				
1145		1150		1155
Lys Asp Arg Ser Cys Tyr Ile Cys His Arg Gln Leu Leu Phe Cys				
1160		1165		1170
Arg Val Thr Leu Gly Lys Ser Phe Leu Gln Phe Ser Ala Met Lys				
1175		1180		1185
Met Ala His Ser Pro Pro Gly His His Ser Val Thr Gly Arg Pro				
1190		1195		1200
Ser Val Asn Gly Leu Ala Leu Ala Glu Tyr Val Ile Tyr Arg Gly				
1205		1210		1215
Glu Gln Ala Tyr Pro Glu Tyr Leu Ile Thr Tyr Gln Ile Met Arg				
1220		1225		1230
Pro Glu Gly Met Val Asp Gly				
1235		1240		

<210> 5  
 <211> 61  
 <212> DNA  
 <213> Homo sapiens

<400> 5  
 gtggaacaga ggggtgcttcc agtttggaga aaaaggaggt tccaggagta gattttagca 60  
 t 61

<210> 6  
 <211> 61  
 <212> DNA  
 <213> Homo sapiens

<400> 6  
 atgcagggga tggcgccgcg ggaacagaaa ggaaggaagg agaagttgct ggtcttgaca 60  
 t 61

<210> 7  
 <211> 20  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> synthetic

<400> 7  
 gtggaacaga ggggtgcttcc 20

<210> 8  
 <211> 583  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> synthetic mutant

<400> 8

Gly Phe Gly Arg Lys Asp Val Val Glu Tyr Leu Leu Gln Asn Gly Ala  
 1 5 10 15

Ser Val Gln Ala Arg Asp Asp Gly Gly Leu Ile Pro Leu His Asn Ala  
 20 25 30

Cys Ser Phe Gly His Ala Glu Val Val Asn Leu Leu Leu Arg His Gly  
 35 40 45

Ala Asp Pro Asn Ala Arg Asp Asn Trp Asn Tyr Thr Pro Leu His Glu  
 50 55 60

Ala Ala Ile Lys Gly Lys Ile Asp Val Cys Ile Val Leu Leu Gln His  
 65 70 75 80

Gly Ala Glu Pro Thr Ile Arg Asn Thr Asp Gly Arg Thr Ala Leu Asp  
 85 90 95

Leu Ala Asp Pro Ser Ala Lys Ala Val Leu Thr Gly Glu Tyr Lys Lys  
 100 105 110

B5  
 Cont.

Asp Glu Leu Leu Glu Ser Ala Arg Ser Gly Asn Glu Glu Lys Met Met  
115 120 125

Ala Leu Leu Thr Pro Leu Asn Val Asn Cys His Ala Ser Asp Gly Arg  
130 135 140

Lys Ser Thr Pro Leu His Leu Ala Ala Gly Tyr Asn Arg Val Lys Ile  
145 150 155 160

Val Gln Leu Leu Leu Gln His Gly Ala Asp Val His Ala Lys Asp Lys  
165 170 175

Gly Asp Leu Val Pro Leu His Asn Ala Cys Ser Tyr Gly His Tyr Glu  
180 185 190

Val Thr Glu Leu Leu Val Lys His Gly Ala Cys Val Asn Ala Met Asp  
195 200 205

Leu Trp Gln Phe Thr Pro Leu His Glu Ala Ala Ser Lys Asn Arg Val  
210 215 220

Glu Val Cys Ser Leu Leu Leu Ser Tyr Gly Ala Asp Pro Thr Leu Leu  
225 230 235 240

Asn Cys His Asn Lys Ser Ala Ile Asp Leu Ala Pro Thr Pro Gln Leu  
245 250 255

Lys Glu Arg Leu Ala Tyr Glu Phe Lys Gly His Ser Leu Leu Gln Ala  
260 265 270

Ala Arg Glu Ala Asp Val Thr Arg Ile Lys Lys His Leu Ser Leu Glu  
275 280 285

Met Val Asn Phe Lys His Pro Gln Thr His Glu Thr Ala Leu His Cys  
290 295 300

Ala Ala Ala Ser Pro Tyr Pro Lys Arg Lys Gln Ile Cys Glu Leu Leu  
305 310 315 320

Leu Arg Lys Gly Ala Asn Ile Asn Glu Lys Thr Lys Glu Phe Leu Thr  
325 330 335

Pro Leu His Val Ala Ser Glu Lys Ala His Asn Asp Val Val Glu Val  
340 345 350

B5  
Cont.

Val Val Lys His Glu Ala Lys Val Asn Ala Leu Asp Asn Leu Gly Gln  
355 360 365

Thr Ser Leu His Arg Ala Ala Tyr Cys Gly His Leu Gln Thr Cys Arg  
370 375 380

Leu Leu Leu Ser Tyr Gly Cys Asp Pro Asn Ile Ile Ser Leu Gln Gly  
385 390 395 400

Phe Thr Ala Leu Gln Met Gly Asn Glu Asn Val Gln Gln Leu Leu Gln  
405 410 415

Glu Gly Ile Ser Leu Gly Asn Ser Glu Ala Asp Arg Gln Leu Leu Glu  
420 425 430

Ala Ala Lys Ala Gly Asp Val Glu Thr Val Lys Lys Leu Cys Thr Val  
435 440 445

Gln Ser Val Asn Cys Arg Asp Ile Glu Gly Arg Gln Ser Thr Pro Leu  
450 455 460

His Phe Ala Ala Gly Tyr Asn Arg Val Ser Val Val Glu Tyr Leu Leu  
465 470 475 480

Gln His Gly Ala Asp Val His Ala Lys Asp Lys Gly Gly Leu Val Pro  
485 490 495

Leu His Asn Ala Cys Ser Tyr Gly His Tyr Glu Val Ala Glu Leu Leu  
500 505 510

Val Lys His Gly Ala Val Val Asn Val Ala Asp Leu Trp Lys Phe Thr  
515 520 525

Pro Leu His Glu Ala Ala Ala Lys Gly Lys Tyr Glu Ile Cys Lys Leu  
530 535 540

Leu Leu Gln His Gly Ala Asp Pro Thr Lys Lys Thr Gly Met Glu Ile  
545 550 555 560

Leu Leu Trp Ile Leu Leu Lys Met Glu Ile Gln Ile Phe Lys Ile Cys  
565 570 575

Leu Gly Glu Met Gln Leu Cys  
580

<210> 9

<211> 1100  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> synthetic mutant

<400> 9

Gly Phe Gly Arg Lys Asp Val Val Glu Tyr Leu Leu Gln Asn Gly Ala  
 1 5 10 15

Ser Val Gln Ala Arg Asp Asp Gly Gly Leu Ile Pro Leu His Asn Ala  
 20 25 30

Cys Ser Phe Gly His Ala Glu Val Val Asn Leu Leu Leu Arg His Gly  
 35 40 45

Ala Asp Pro Asn Ala Arg Asp Asn Trp Asn Tyr Thr Pro Leu His Glu  
 50 55 60

Ala Ala Ile Lys Gly Lys Ile Asp Val Cys Ile Val Leu Leu Gln His  
 65 70 75 80

Gly Ala Glu Pro Thr Ile Arg Asn Thr Asp Gly Arg Thr Ala Leu Asp  
 85 90 95

Leu Ala Asp Pro Ser Ala Lys Ala Val Leu Thr Gly Glu Tyr Lys Lys  
 100 105 110

Asp Glu Leu Leu Glu Ser Ala Arg Ser Gly Asn Glu Glu Lys Met Met  
 115 120 125

Ala Leu Leu Thr Pro Leu Asn Val Asn Cys His Ala Ser Asp Gly Arg  
 130 135 140

Lys Ser Thr Pro Leu His Leu Ala Ala Gly Tyr Asn Arg Val Lys Ile  
 145 150 155 160

Val Gln Leu Leu Leu Gln His Gly Ala Asp Val His Ala Lys Asp Lys  
 165 170 175

Gly Asp Leu Val Pro Leu His Asn Ala Cys Ser Tyr Gly His Tyr Glu  
 180 185 190

Val Thr Glu Leu Leu Val Lys His Gly Ala Cys Val Asn Ala Met Asp  
 195 200 205

B5  
 Cont.

Leu Trp Gln Phe Thr Pro Leu His Glu Ala Ala Ser Lys Asn Arg Val  
 210 215 220

Glu Val Cys Ser Leu Leu Leu Ser Tyr Gly Ala Asp Pro Thr Leu Leu  
 225 230 235 240

Asn Cys His Asn Lys Ser Ala Ile Asp Leu Ala Pro Thr Pro Gln Leu  
 245 250 255

Lys Glu Arg Leu Ala Tyr Glu Phe Lys Gly His Ser Leu Leu Gln Ala  
 260 265 270

Ala Arg Glu Ala Asp Val Thr Arg Ile Lys Lys His Leu Ser Leu Glu  
 275 280 285

Met Val Asn Phe Lys His Pro Gln Thr His Glu Thr Ala Leu His Cys  
 290 295 300

Ala Ala Ala Ser Pro Tyr Pro Lys Arg Lys Gln Ile Cys Glu Leu Leu  
 305 310 315 320

Leu Arg Lys Gly Ala Asn Ile Asn Glu Lys Thr Lys Glu Phe Leu Thr  
 325 330 335

Pro Leu His Val Ala Ser Glu Lys Ala His Asn Asp Val Val Glu Val  
 340 345 350

Val Val Lys His Glu Ala Lys Val Asn Ala Leu Asp Asn Leu Gly Gln  
 355 360 365

Thr Ser Leu His Arg Ala Ala Tyr Cys Gly His Leu Gln Thr Cys Arg  
 370 375 380

Leu Leu Leu Ser Tyr Gly Cys Asp Pro Asn Ile Ile Ser Leu Gln Gly  
 385 390 395 400

Phe Thr Ala Leu Gln Met Gly Asn Glu Asn Val Gln Gln Leu Leu Gln  
 405 410 415

Glu Gly Ile Ser Leu Gly Asn Ser Glu Ala Asp Arg Gln Leu Leu Glu  
 420 425 430

Ala Ala Lys Ala Gly Asp Val Glu Thr Val Lys Lys Leu Cys Thr Val  
 435 440 445

Gln Ser Val Asn Cys Arg Asp Ile Glu Gly Arg Gln Ser Thr Pro Leu

B5  
 cont.

450

455

460

His Phe Ala Ala Gly Tyr Asn Arg Val Ser Val Val Glu Tyr Leu Leu  
 465 470 475 480

Gln His Gly Ala Asp Val His Ala Lys Asp Lys Gly Gly Leu Val Pro  
 485 490 495

Leu His Asn Ala Cys Ser Tyr Gly His Tyr Glu Val Ala Glu Leu Leu  
 500 505 510

Val Lys His Gly Ala Val Val Asn Val Ala Asp Leu Trp Lys Phe Thr  
 515 520 525

Pro Leu His Glu Ala Ala Ala Lys Gly Lys Tyr Glu Ile Cys Lys Leu  
 530 535 540

Leu Leu Gln His Gly Ala Asp Pro Thr Lys Lys Asn Arg Asp Gly Asn  
 545 550 555 560

Thr Pro Leu Asp Leu Val Lys Asp Gly Asp Thr Asp Ile Gln Asp Leu  
 565 570 575

Leu Arg Gly Asp Ala Ala Leu Leu Asp Ala Ala Lys Lys Gly Cys Leu  
 580 585 590

Ala Arg Val Lys Lys Leu Ser Ser Pro Asp Asn Val Asn Cys Arg Asp  
 595 600 605

Thr Gln Gly Arg His Ser Thr Pro Leu His Leu Ala Ala Gly Tyr Asn  
 610 615 620

Asn Leu Glu Val Ala Glu Tyr Leu Leu Gln His Gly Ala Asp Val Asn  
 625 630 635 640

Ala Gln Asp Lys Gly Gly Leu Ile Pro Leu His Asn Ala Ala Ser Tyr  
 645 650 655

Gly His Val Asp Val Ala Ala Leu Leu Ile Lys Tyr Asn Ala Cys Val  
 660 665 670

Asn Ala Thr Asp Lys Trp Ala Phe Thr Pro Leu His Glu Ala Ala Gln  
 675 680 685

Lys Gly Arg Thr Gln Leu Cys Ala Leu Leu Leu Ala His Gly Ala Asp  
 690 695 700

Pro Thr Leu Lys Asn Gln Glu Gly Gln Thr Pro Leu Asp Leu Val Ser  
705 710 715 720

Ala Asp Asp Val Ser Ala Leu Leu Thr Ala Ala Met Pro Pro Ser Ala  
725 730 735

Leu Pro Ser Cys Tyr Lys Pro Gln Val Leu Asn Gly Val Arg Ser Pro  
740 745 750

Gly Ala Thr Ala Asp Ala Leu Ser Ser Gly Pro Ser Ser Pro Ser Ser  
755 760 765

Leu Ser Ala Ala Ser Ser Leu Asp Asn Leu Ser Gly Ser Phe Ser Glu  
770 775 780

Leu Ser Ser Val Val Ser Ser Ser Gly Thr Glu Gly Ala Ser Ser Leu  
785 790 795 800

Glu Lys Lys Glu Val Pro Gly Val Asp Phe Ser Ile Thr Gln Phe Val  
805 810 815

Arg Asn Leu Gly Leu Glu His Leu Met Asp Ile Phe Glu Arg Glu Gln  
820 825 830

Ile Thr Leu Asp Val Leu Val Glu Met Gly His Lys Glu Leu Lys Glu  
835 840 845

Ile Gly Ile Asn Ala Tyr Gly His Arg His Lys Leu Ile Lys Gly Val  
850 855 860

Glu Arg Leu Ile Ser Gly Gln Gln Gly Leu Asn Pro Tyr Leu Thr Leu  
865 870 875 880

Asn Thr Ser Gly Ser Gly Thr Ile Leu Ile Asp Leu Ser Pro Asp Asp  
885 890 895

Lys Glu Phe Gln Ser Val Glu Glu Glu Met Gln Ser Thr Val Arg Glu  
900 905 910

His Arg Asp Gly Gly His Ala Gly Gly Ile Phe Asn Arg Tyr Asn Ile  
915 920 925

Leu Lys Ile Gln Lys Val Cys Asn Lys Lys Leu Trp Glu Arg Tyr Thr  
930 935 940

B5  
Cont.

His Arg Arg Lys Glu Val Ser Glu Glu Asn His Asn His Ala Asn Glu  
945 950 955 960

Arg Met Leu Phe His Gly Ser Pro Phe Val Asn Ala Ile Ile His Lys  
965 970 975

Gly Phe Asp Glu Arg His Ala Tyr Ile Gly Gly Met Phe Gly Ala Gly  
980 985 990

Ile Tyr Leu Ala Glu Asn Ser Ser Lys Ser Asn Gln Tyr Val Tyr Gly  
995 1000 1005

Ile Gly Gly Gly Thr Gly Cys Pro Val His Lys Asp Arg Ser Cys  
1010 1015 1020

Tyr Ile Cys His Arg Gln Leu Leu Phe Cys Arg Val Thr Leu Gly  
1025 1030 1035

Lys Ser Phe Leu Gln Phe Ser Ala Met Lys Met Ala His Ser Pro  
1040 1045 1050

Pro Gly His His Ser Val Thr Gly Arg Pro Ser Val Asn Gly Leu  
1055 1060 1065

Ala Leu Ala Glu Tyr Val Ile Tyr Arg Gly Glu Gln Ala Tyr Pro  
1070 1075 1080

Glu Tyr Leu Ile Thr Tyr Gln Ile Met Arg Pro Glu Gly Met Val  
1085 1090 1095

Asp Gly  
1100

<210> 10  
<211> 1083  
<212> PRT  
<213> Artificial sequence

<220>  
<223> synthetic mutant

<400> 10

Gly Phe Gly Arg Lys Asp Val Val Glu Tyr Leu Leu Gln Asn Gly Ala  
1 5 10 15

Ser Val Gln Ala Arg Asp Asp Gly Gly Leu Ile Pro Leu His Asn Ala  
20 25 30

Cys Ser Phe Gly His Ala Glu Val Val Asn Leu Leu Leu Arg His Gly  
35 40 45

Ala Asp Pro Asn Ala Arg Asp Asn Trp Asn Tyr Thr Pro Leu His Glu  
50 55 60

Ala Ala Ile Lys Gly Lys Ile Asp Val Cys Ile Val Leu Leu Gln His  
65 70 75 80

Gly Ala Glu Pro Thr Ile Arg Asn Thr Asp Gly Arg Thr Ala Leu Asp  
85 90 95

Leu Ala Asp Pro Ser Ala Lys Ala Val Leu Thr Gly Glu Tyr Lys Lys  
100 105 110

Asp Glu Leu Leu Glu Ser Ala Arg Ser Gly Asn Glu Glu Lys Met Met  
115 120 125

Ala Leu Leu Thr Pro Leu Asn Val Asn Cys His Ala Ser Asp Gly Arg  
130 135 140

Lys Ser Thr Pro Leu His Leu Ala Ala Gly Tyr Asn Arg Val Lys Ile  
145 150 155 160

Val Gln Leu Leu Leu Gln His Gly Ala Asp Val His Ala Lys Asp Lys  
165 170 175

Gly Asp Leu Val Pro Leu His Asn Ala Cys Ser Tyr Gly His Tyr Glu  
180 185 190

Val Thr Glu Leu Leu Val Lys His Gly Ala Cys Val Asn Ala Met Asp  
195 200 205

Leu Trp Gln Phe Thr Pro Leu His Glu Ala Ala Ser Lys Asn Arg Val  
210 215 220

Glu Val Cys Ser Leu Leu Leu Ser Tyr Gly Ala Asp Pro Thr Leu Leu  
225 230 235 240

Asn Cys His Asn Lys Ser Ala Ile Asp Leu Ala Pro Thr Pro Gln Leu  
245 250 255

Lys Glu Arg Leu Ala Tyr Glu Phe Lys Gly His Ser Leu Leu Gln Ala  
260 265 270

Ala Arg Glu Ala Asp Val Thr Arg Ile Lys Lys His Leu Ser Leu Glu  
275 280 285

Met Val Asn Phe Lys His Pro Gln Thr His Glu Thr Ala Leu His Cys  
290 295 300

Ala Ala Ala Ser Pro Tyr Pro Lys Arg Lys Gln Ile Cys Glu Leu Leu  
305 310 315 320

Leu Arg Lys Gly Ala Asn Ile Asn Glu Lys Thr Lys Glu Phe Leu Thr  
325 330 335

Pro Leu His Val Ala Ser Glu Lys Ala His Asn Asp Val Val Glu Val  
340 345 350

Val Val Lys His Glu Ala Lys Val Asn Ala Leu Asp Asn Leu Gly Gln  
355 360 365

Thr Ser Leu His Arg Ala Ala Tyr Cys Gly His Leu Gln Thr Cys Arg  
370 375 380

Leu Leu Leu Ser Tyr Gly Cys Asp Pro Asn Ile Ile Ser Leu Gln Gly  
385 390 395 400

Phe Thr Ala Leu Gln Met Gly Asn Glu Asn Val Gln Gln Leu Leu Gln  
405 410 415

Glu Gly Ile Ser Leu Gly Asn Ser Glu Ala Asp Arg Gln Leu Leu Glu  
420 425 430

Ala Ala Lys Ala Gly Asp Val Glu Thr Val Lys Lys Leu Cys Thr Val  
435 440 445

Gln Ser Val Asn Cys Arg Asp Ile Glu Gly Arg Gln Ser Thr Pro Leu  
450 455 460

His Phe Ala Ala Gly Tyr Asn Arg Val Ser Val Val Glu Tyr Leu Leu  
465 470 475 480

Gln His Gly Ala Asp Val His Ala Lys Asp Lys Gly Gly Leu Val Pro  
485 490 495

Leu His Asn Ala Cys Ser Tyr Gly His Tyr Glu Val Ala Glu Leu Leu  
500 505 510

Val Lys His Gly Ala Val Val Asn Val Ala Asp Leu Trp Lys Phe Thr  
515 520 525

Pro Leu His Glu Ala Ala Ala Lys Gly Lys Tyr Glu Ile Cys Lys Leu  
530 535 540

Leu Leu Gln His Gly Ala Asp Pro Thr Lys Lys Asn Arg Asp Gly Asn  
545 550 555 560

Thr Pro Leu Asp Leu Val Lys Asp Gly Asp Thr Asp Ile Gln Asp Leu  
565 570 575

Leu Arg Gly Asp Ala Ala Leu Leu Asp Ala Ala Lys Lys Gly Cys Leu  
580 585 590

Ala Arg Val Lys Lys Leu Ser Ser Pro Asp Asn Val Asn Cys Arg Asp  
595 600 605

Thr Gln Gly Arg His Ser Thr Pro Leu His Leu Ala Ala Gly Tyr Asn  
610 615 620

Asn Leu Glu Val Ala Glu Tyr Leu Leu Gln His Gly Ala Asp Val Asn  
625 630 635 640

Ala Gln Asp Lys Gly Gly Leu Ile Pro Leu His Asn Ala Ala Ser Tyr  
645 650 655

Gly His Val Asp Val Ala Ala Leu Leu Ile Lys Tyr Asn Ala Cys Val  
660 665 670

Asn Ala Thr Asp Lys Trp Ala Phe Thr Pro Leu His Glu Ala Ala Gln  
675 680 685

Lys Gly Arg Thr Gln Leu Cys Ala Leu Leu Leu Ala His Gly Ala Asp  
690 695 700

Pro Thr Leu Lys Asn Gln Glu Gly Gln Thr Pro Leu Asp Leu Val Ser  
705 710 715 720

Ala Asp Asp Val Ser Ala Leu Leu Thr Ala Ala Met Pro Pro Ser Ala  
725 730 735

Leu Pro Ser Cys Tyr Lys Pro Gln Val Leu Asn Gly Val Arg Ser Pro  
740 745 750

Gly Ala Thr Ala Asp Ala Leu Ser Ser Gly Pro Ser Ser Pro Ser Ser

755

760

765

Leu Ser Ala Ala Ser Ser Leu Asp Asn Leu Ser Gly Ser Phe Ser Glu  
 770 775 780

Leu Ser Ser Val Val Ser Ser Ser Gly Thr Glu Gly Ala Ser Ser Leu  
 785 790 795 800

Glu Lys Lys Glu Val Pro Gly Val Asp Phe Ser Ile Thr Gln Phe Val  
 805 810 815

Arg Asn Leu Gly Leu Glu His Leu Met Asp Ile Phe Glu Arg Glu Gln  
 820 825 830

Ile Thr Leu Asp Val Leu Val Glu Met Gly His Lys Glu Leu Lys Glu  
 835 840 845

Ile Gly Ile Asn Ala Tyr Gly His Arg His Lys Leu Ile Lys Gly Val  
 850 855 860

Glu Arg Leu Ile Ser Gly Gln Gln Gly Leu Asn Pro Tyr Leu Thr Leu  
 865 870 875 880

Asn Thr Ser Gly Ser Gly Thr Ile Leu Ile Asp Leu Ser Pro Asp Asp  
 885 890 895

Lys Glu Phe Gln Ser Val Glu Glu Glu Met Gln Ser Thr Val Arg Glu  
 900 905 910

His Arg Asp Gly Gly His Ala Gly Gly Ile Phe Asn Arg Tyr Asn Ile  
 915 920 925

Leu Lys Ile Gln Lys Val Cys Asn Lys Lys Leu Trp Glu Arg Tyr Thr  
 930 935 940

His Arg Arg Lys Glu Val Ser Glu Glu Asn His Asn His Ala Asn Glu  
 945 950 955 960

Arg Met Leu Phe His Gly Ser Pro Phe Val Asn Ala Ile Ile His Lys  
 965 970 975

Gly Phe Asp Glu Arg His Ala Tyr Ile Gly Gly Met Phe Gly Ala Gly  
 980 985 990

Ile Tyr Phe Ala Glu Asn Ser Ser Lys Ser Asn Gln Tyr Val Tyr Gly  
 995 1000 1005

Ile Gly Gly Gly Thr Gly Cys Pro Val His Lys Asp Arg Ser Cys  
1010 1015 1020

Tyr Ile Cys His Arg Gln Leu Leu Phe Cys Arg Val Thr Leu Gly  
1025 1030 1035

Lys Ser Phe Leu Gln Phe Ser Ala Met Lys Met Ala His Ser Pro  
1040 1045 1050

Pro Gly His His Ser Val Thr Gly Arg Pro Ser Val Asn Gly Leu  
1055 1060 1065

Ala Leu Ala Ala Tyr Val Ile Tyr Arg Gly Glu Gln Ala Leu Ser  
1070 1075 1080

<210> 11  
<211> 9  
<212> PRT  
<213> Unknown

<220>  
<223> cyclin A destruction box

<400> 11

Arg Thr Val Leu Gly Val Ile Gly Asp  
1 5

<210> 12  
<211> 9  
<212> PRT  
<213> Unknown

<220>  
<223> Cyclin B1 destruction box

<400> 12

Arg Thr Ala Leu Gly Asp Ile Gly Asn  
1 5

<210> 13  
<211> 27  
<212> PRT  
<213> Rattus sp.

<400> 13

Tyr Met Thr Val Ser Ile Ile Asp Arg Phe Met Gln Asp Ser Cys Val  
1 5 10 15

Pro Lys Lys Met Leu Gln Leu Val Gly Val Thr  
20 25

<210> 14  
<211> 28  
<212> PRT  
<213> Mus sp.

<400> 14

Lys Phe Arg Leu Leu Gln Glu Thr Met Tyr Met Thr Val Ser Ile Ile  
1 5 10 15

Asp Arg Phe Met Gln Asn Ser Cys Val Pro Lys Lys  
20 25

<210> 15  
<211> 27  
<212> PRT  
<213> Mus sp.

<400> 15

Arg Ala Ile Leu Ile Asp Trp Leu Ile Gln Val Gln Met Lys Phe Arg  
1 5 10 15

Leu Leu Gln Glu Thr Met Tyr Met Thr Val Ser  
20 25

<210> 16  
<211> 27  
<212> PRT  
<213> Mus sp.

<400> 16

Asp Arg Phe Leu Gln Ala Gln Leu Val Cys Arg Lys Lys Leu Gln Val  
1 5 10 15

Val Gly Ile Thr Ala Leu Leu Leu Ala Ser Lys  
20 25

<210> 17  
<211> 18  
<212> PRT  
<213> Mus sp.

<400> 17

Met Ser Val Leu Arg Gly Lys Leu Gln Leu Val Gly Thr Ala Ala Met  
1 5 10 15

Leu Leu